==========

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=11; day=4; hr=9; min=21; sec=49; ms=542;]

==========

****

Reviewer Comments:

<160> 66

Although the above <160> response is "66", 68 sequences are in the submitted file. Please see below:

<210> 68

<211> 10

<212> PRT

<213> Saccharomyces cerevisiae

<400> 68

Glu Arg Trp Ile Trp Ile Arg Ser Gly Thr

1 5 10

The above is the last sequence in the submitted file.

****

Validated By CRFValidator v 1.0.3

Application No: 10575374 Version No: 2.0

Input Set:

Output Set:

Started: 2009-10-21 17:32:28.305
Finished: 2009-10-21 17:32:30.540
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 235 ms
Total Warnings: 48
Total Errors: 2
No. of SeqIDs Defined: 66
Actual SeqID Count: 68

Error code		Error Description
E	257	Invalid sequence data feature in <221> in SEQ ID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)
W	213	Artificial or Unknown found in <213> in SEQ ID (21)
W	213	Artificial or Unknown found in <213> in SEQ ID (22)
W	213	Artificial or Unknown found in <213> in SEQ ID (23)
W	213	Artificial or Unknown found in <213> in SEQ ID (24)
W	213	Artificial or Unknown found in <213> in SEQ ID (25)
W	213	Artificial or Unknown found in <213> in SEQ ID (26)
W	213	Artificial or Unknown found in <213> in SEQ ID (27)
W	213	Artificial or Unknown found in <213> in SEQ ID (28)
W	213	Artificial or Unknown found in <213> in SEQ ID (29)
W	213	Artificial or Unknown found in <213> in SEQ ID (30)
W	213	Artificial or Unknown found in <213> in SEQ ID (31)
W	213	Artificial or Unknown found in <213> in SEQ ID (32)
W	213	Artificial or Unknown found in <213> in SEQ ID (33)
W	213	Artificial or Unknown found in <213> in SEQ ID (34)
W	213	Artificial or Unknown found in <213> in SEQ ID (35)
W	213	Artificial or Unknown found in <213> in SEQ ID (36)
W	213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2009-10-21 17:32:28.305
Finished: 2009-10-21 17:32:30.540
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 235 ms
Total Warnings: 48
Total Errors: 2
No. of SeqIDs Defined: 66
Actual SeqID Count: 68

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38) This error has occured more than 20 times, will not be displayed
E 252	Calc# of Seq. differs from actual; 66 seqIds defined; count=68

SEQUENCE LISTING

<110> Ecole Polytechnique Federale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<140> 10575374
<141> 2009-10-21

<150> US 34,404 JM-213
<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1
<211> 672
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> modified_base
<222> (186)..(186)
<223> silent point mutation introduced to generate HindIII restriction site

<300>
<308> NCBI / NC_001136
<309> 2004-08-30

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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180

aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa 240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc 360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600

agcggaggtg tggagacaaa tggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa 660

<210> 2
<211> 224
<212> PRT
<213> Saccharomyces cerevisiae

<300>
<308> NCBI / NC_001136
<309> 2004-08-30

<400> 2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

```
Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
            180                 185                 190


Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
        195                 200                 205


Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
    210                 215                 220


<210>  3
<211>  132
<212>  DNA
<213>  Saccharomyces cerevisiae

<220>
<221>  modified_base
<222>  (22)..(22)
<223>  point mutation


<400>  3
atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag     60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt    120

gtgcccaata ga                                                        132


<210>  4
<211>  44
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1               5                   10                  15


Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20                  25                  30


Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
        35                  40


<210>  5
<211>  540
<212>  DNA
<213>  Saccharomyces cerevisiae
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<400> 5
aagagaacaa ttgacccggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa 60

aatagttcag gcactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120

gttttggctc tggtcaatga ttacggcatt gatatcgtcc aactgcacgg agatgagtcg 180

tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa 240

gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt 300

gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactgggtt 360

ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa 420

aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg 480

gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6
<211> 180
<212> PRT
<213> Saccharomyces cerevisiae

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser
115 120 125

```
Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
    130                 135                 140


Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145                 150                 155                 160


Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
                165                 170                 175


Asn Ala Lys Lys
            180


<210>  7
<211>  159
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  7
atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag     60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt    120

gtgcccaata gaaagagaac aattgacccg gttattgca                           159


<210>  8
<211>  53
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1               5                   10                  15


Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20                  25                  30


Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35                  40                  45


Asp Pro Val Ile Ala
    50


<210>  9
<211>  516
<212>  DNA
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<213> Saccharomyces cerevisiae

<400> 9

gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac 60

ttggttggcg tgtttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac 120

ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc 180

ggtttgccag ttattaaaag actcgtattt ccaaaagact gcaacatact actcagtgca 240

gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt 300

gaacttttgg attggaactc gatttctgac tgggttggaa ggcaagagag ccccgagagc 360

ttacatttta tgttagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta 420

aatggcgtta ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct 480

aacaaaatag caaatttcgt caaaaatgct aagaaa 516

<210> 10
<211> 172
<212> PRT
<213> Saccharomyces cerevisiae

<400> 10

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1 5 10 15

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
20 25 30

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
35 40 45

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
50 55 60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65 70 75 80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
85 90 95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
100 105 110

```
Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
        115                 120                 125


Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
    130                 135                 140


Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
145                 150                 155                 160


Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
                165                 170


<210>  11
<211>  561
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  11
atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag     60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt    120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta    180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa    240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac    300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc    360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt    420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt    480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga    540

ctgacgccag aaaatgttgg t                                               561


<210>  12
<211>  187
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1               5                   10                  15


Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20                  25                  30
```

```
Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35                  40                  45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
    50                  55                  60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65                  70                  75                  80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
                85                  90                  95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
            100                 105                 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
        115                 120                 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
    130                 135                 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145                 150                 155                 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
                165                 170                 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
            180                 185


<210>  13
<211>  111
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  13
gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat     60

ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a             111


<210>  14
<211>  37
<212>  PRT
<213>  Saccharomyces cerevisiae
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<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
20 25 30

Lys Asn Ala Lys Lys
35

<210> 15
<211> 612
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> mutation
<222> (22)..(22)
<223> point mutation

<220>
<221> deletion
<222> (612)..(612)
<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAAAG
ACTCT

<400> 15
atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag 60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa 240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc 360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600

agcggaggtg tg 612

<210> 16

<211> 204
<212> PRT
<213> Saccharomyces cerevisiae

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
195 200

<210> 17
<211> 36
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> mutation
<222> (1)..(1)
<223> missing sequence before base 1 of SEQ17, corresponding to base 63
7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17
aacaaaatag caaatttcgt caaaaatgct aagaaa 36

<210> 18
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
1 5 10

<210> 19
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> first of a pair of peptides (together with peptide C2), that asso
ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),
12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
35 40

<210> 20
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp